

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/915 706

Source: OIPE

Date Processed by STIC: 10/17/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/915706</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENCLISII "ALPIIA" HEADERS, WIICII WERE INSERTED BY I		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 3 rd amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (i) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (ii) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (iii) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID.NO where "X" is shown) This sequence is intentionally skipped	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequence: Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequence: <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rule)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/915,706

DATE: 10/17/2001
TIME: 15:54:53

Input Set : A:\5112.app
Output Set: N:\CRF3\10172001\I915706.raw

3 <110> APPLICANT: NELSON, DAVID R.
5 <120> TITLE OF INVENTION: A LIVE, AVIRULENT STRAIN OF V. ANGUILLARUM THAT
6 PROTECTS FISH AGAINST INFECTION BY VIRULENT V.
7 ANGUILLARUM
9 <130> FILE REFERENCE: 5112
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/915,706 ✓
C--> 12 <141> CURRENT FILING DATE: 2001-07-26 ✓
14 <160> NUMBER OF SEQ ID NOS: 4
16 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
Corrected File Date Needed

ERRORED SEQUENCES

18 <210> SEQ ID NO: 1
19 <211> LENGTH: 3609
20 <212> TYPE: DNA
21 <213> ORGANISM: V. Anguillarum
23 <220> FEATURE:
24 <223> OTHER INFORMATION: "n" bases may be a, t, c, g, other or unknown
26 <400> SEQUENCE: 1
27 gtcgacttat tgcattgatg gcgtacatgg tagtgcatac cttcggttgc taacaaggcg 60
28 tgtataaaag ctgggtcggt ttcatcaagt tgaacacaaat actcatgatt ttcccaactt 120
29 ccgaaaaggg aaaagtaaaa atagctttt agatcagcct gttcttagcag ctttcaatg 180
30 atcttttcg tcgttacgtt ttgaaaaatc tgacgactgc gtttgtattt caacaagcta 240
31 agtggatcca atatcttat ttgataataa aactgtcgct tgcctttgc atatccgtg 300
32 aattgcagag tgctacatat acctaaaaaa aaacgcgttc cagaatctaa ttcgttaagac 360
33 acacaaacag ctttacctag gttttggta tcgatctcca tgtttgcgc gatggaaacg 420
34 gaaaactgac acccgccgga tacgctttcc tctccgatta attgcgtgac aatataactt 480
35 ttgctatctg aaagcttaat ggtgagggag cgggttgggt gctttaattc gttactgctc 540
36 atattcaatt aattcactat taaataaaaca gttctaaaag gctgtttatt ggatgaatat 600
37 tcgaaattat cacataataa ttgatgctat tattacttgc ttttggta tcaactttca 660
38 tgctctatac atgtaataata tttcgagttt gaccttaattt caaggttattt tgccttattt 720
39 attattatct gaataatatg taatcgattt ctttgggtt atttttatgt ttgtttcatt 780
40 tttaatgacg gtgagctgt gcattcatat ttatgtat gacaacatct ttgatgaagt 840
41 atttaagata ttgttaatgc atgaggggtt tgcgtgtattt ttatatttta aatcataata 900
42 aaatcaacaa tatatgttat ttttgttctt ttatagtgt tcttttaaag aggttaggatg 960
43 acctaaagggt cgcctagaaaa tatggcgtaa attgccattt ctataattca cctcaaagat 1020
44 acactattgg caaatgtaca aatatgtcac ttctgtatgaa acaatatttg tagatgtgt 1080
45 tttgtctgca aaaataaaaaa ttttctgtt tgaaataactt caaggcctct agcggtttcc 1140
46 ttatcttaa aatacaggaa atagcgattt aagtttattt acacttaagg aasdramgaa 1200
47 tagtcaaccc aacagagcag gaaacctatgc ctttgcataa gcatcaaattt gagcaacttt 1260
48 ctaaacctct gaggatgtat tcgtatgtt gctttatct taaaactggaa aaaagtgcctt 1320
49 ttgcgcattt acgtaatgaa ttatgtcg cgaaactgc gctgcgttaag ctaagtcaaa 1380
50 acccttagtc tgacgagaga gatgcgttac aagaggcatg tctaaataag tggaaagattc 1440
51 tctctgacag ttgtacgaa cagtttcaa aaacaaccag agatatcgag ctcatctcat 1500
52 ggtttggcgc tgctcaattt cttctcgata ccacattaga aagtgcgtcg aatagcctt 1560
53 agtggtagc ggatthaagt gagaaggactt caaccctgtt ctaccagtt 1620

See page 2 of 4

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54	aaacgctcaa atctgtat gataaggca aagaaagaga gcaagcagat gcgaaagtta	1680
55	aacattttt ccaactagtc ggcgatagcg agggaaagctc gattcttat gcgcgggtgc	1740
56	tgcactgcc cttagtcggg gaagtgcgt ttttgactt tcaaagtgcg gagagaaaag	1800
57	gcgaaatcag ccaactgaaa tctatgccta cgaccacggt ggcgcaagag cgtttcgca	1860
58	ttcaattcaa gatggaaaac gccaaacgtt gtgtcaccca attagatcgt ttgtcagcgt	1920
59	tggtagcac taagtgcata tctctaggca gtc当地gatac caacttcgga ttgcgaaat	1980
60	cactgcttac ccgtgtgaa aacgcttgg ttcatacg tggaaattaag ttagcaccga	2040
61	aagcggaggc caagacagta gagcaagagg ttgc当地aaatggggagc	2100
62	tgccaagcca tatggataca aaacatatacg agcgaatacc gatggcatca ggc当地ggctc	2160
63	agaccgtaaag ccaacactta cacgcaggaa acctctctgaa actggtaat taaacaata	2220
64	tgaaccgaga ct当地gcttc catttggta gagaagtc当地 tgattatgg cggc当地agagcg	2280
65	aaccgc当地at cccaaattca ttttggtag aaaaagcgat tc当地atggggat tatttataat	2340
66	tacctgagtt gctgc当地gaa atgatgtcgg aacaaaacgg tgacgctt当地 agtacgattt	2400
67	ttaatgccc当地 cggattgaaat catctcgatc aggtttgct gccggaggta agtactccaa	2460
68	cggtagccat tggaaaggccc caaacaccc local aagcgaagcc ttccggttgc gatccgc当地a	2520
69	gtgttgaaga gcatgtatct cagacttccc ctgtagatac ccaatctaag caagatcaa	2580
E--> 70	aaccacaatc atccgctt* drbcgtcggc tctgagttgg taattgtgtt taaaaataa	2640
71	ggaaaaatca tggcaagttt ttaatgcgt gtaagcggc ttcaagttga gggc当地cagcg	2700
72	actatcggtc agctagaaaac ggctgaaggt aaaaatgacg gttgggttgc aatcaactct	2760
73	tactcttggg gtggc当地ctcg taacggttgc atggacatcg gtaacggc当地 caatcggtat	2820
74	tcaggcatgg ttggcgtaaag cgaagtttagc gtaactaaag aagtgc当地tgg tgcttctgaa	2880
75	gacctactgt ct当地tattt caacccaggta aagacggtt gaaactgttga ggttgc当地tattt	2940
76	actaaggc当地tta acacgtatgg tcaagggtc当地 gacgtt当地act tccaaatgtt当地 gctagaaaaaa	3000
77	gcacgtt当地tag ttctt当地aca cgtgacggg actgacggat ctcaaccgtt gggc当地cagcg	3060
78	tcttttctt acacttctat ttctc当地agaag catcactatg agaaagaagg tggtaacta	3120
E--> 79	caaagggtg gtgtt当地gac ttacgaccta cc当地gaggaa aaaaatgactt ctggtaacta	3180
80	attctt当地cat tagacatgcc acgtt当地attt gcatgtctat ttcatgaaata tctcsdrlocal	3240
81	tttaggacac cgttatggca ttgaactc当地 aacataagcg cgttagtaag aaccgtgtca	3300
82	gcatcaccta tgacgtt当地 aacaaatggcg cc当地aaagac gaaagagctg cc当地tgggtt当地	3360
83	ttggc当地tcat tggcactt当地 tcaggacaca aaccagaatc agaaaaatgtt gatttagaag	3420
84	agcagagttt cacgggtatc gataaaagaca acttc当地atc agtgc当地tggg caaatcacc	3480
85	cgc当地tcttc gtacaaggat gataacaago ttgctaaatgat gtagccag ttgaagtga	3540
W--> 86	acttgagcc local ccgtt当地gatg aaagatttcc acccagagaa ct当地gtt当地gatnnaatgagc	3600
87	cgcttaaag	3609

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors. Specifically Sequence 4.

Sequence 1 Errors:
n's must be enumerated
in fields 221, 222 and
223.

1. Field 221 must be "unseen"
2. Field 222 must be a location in the sequence
3. Field 223 must be n = some string of possible unknowns

VERIFICATION SUMMARY

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Output Set: N:\CRF3\10172001\I915706.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:70 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:79 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:86 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:86 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:86 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:253 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:253 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:253 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

<400> 4

Met Ala Leu Asn Ser Gln His Lys Arg Val Ser Lys Asn Arg Val Ser
1 5 10 15

Ile Thr Tyr Asp Val Glu Thr Asn Gly Ala Val Lys Thr Lys Glu Leu
20 25 30

Pro Phe Val Val Gly Val Ile Gly Asp Phe Ser Gly His Lys Pro Glu
35 40 45

Ser Glu Lys Val Asp Leu Glu Glu Arg Glu Phe Thr Gly Ile Asp Lys
50 55 60

Asp Asn Phe Asp Thr Val Met Gly Gln Ile His Pro Arg Leu Ser Tyr
65 70 75 80

Lys Val Asp Asn Lys Leu Ala Asn Asp Asp Ser Gln Phe Glu Val Asn
85 90 95

Leu Ser Leu Arg Ser Met Lys Asp Phe His Pro Glu Asn Leu Val Asp
100 105 110

Xaa Ile Glu Pro Leu
115